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Plant Gene Register

An Apple Gene Highly Expressed in Fruit

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Although apple is an important horticultural crop, its molecular biology is not well understood. Only a few apple genes have thus far been isolated, and these include genes encoding ACC synthase (Dong et al., 1991a) and ACC oxidase (Dong et al., 1991b; Ross et al., 1992) enzymes in the ethylene biosynthetic pathway (Yang and Hoffman, 1984). The identification of other genes controlling important fruit characteristics, and a better understanding of their regulation, would enhance prospects for improving this crop using gene-transfer technology.

We report here a cDNA clone (AP1) that encodes a message highly expressed in apple fruit (*Malus domestica* Borkh. cv Golden Delicious). The clone was isolated from a cDNA library constructed using poly(A)$^+$ RNA from cortical tissue of ripe apple fruit (Ross et al., 1992). The nucleic acid sequence of AP1 is 705 bp and contains an open reading frame encoding a 119-amino acid polypeptide (Table I). This deduced polypeptide is hydrophilic, with 32 charged residues out of 119. Southern analysis indicates that the gene coding for AP1 has a low copy number.

Northern analysis has shown that AP1 expression, although highest in fruit tissue, was also detectable in apple leaf, stem, petiole, seed, and root tissue (our unpublished data). In fruit, AP1 mRNA was detected in a range of developmental stages, from ovaries of flowers at full bloom to ripe fruit.

The AP1 nucleic acid and deduced polypeptide sequence are 66 and 83% identical, respectively, to those of λSAR5, a cDNA clone coding for a strawberry gene that is repressed by exogenously applied auxin (Reddy and Poovaiah, 1990).

Table I. *Characteristics of pAP1 cDNA from apple fruit*

Organism:
Apple (*Malus domestica* Borkh. cv Golden Delicious).
Techniques:
Isolated from a cDNA library in pSPORT1 (Ross et al., 1992). Complete double-stranded cDNA sequence was obtained by dideoxy sequencing of subclones.
Method of Identification:
Nucleotide sequence showed 66% homology with λSAR5 (X52429).
Features of mRNA:
Detected by northern hybridization in fruit, leaf, stem, petiole, root, and seed. Level of mRNA varied during fruit development and was highest in later stages of fruit development and in ripe fruit.
Features of cDNA Clone:
The AP1 cDNA contains 33 nucleotides of 5′ untranslated sequence, an open reading frame 357 nucleotides in length, and 315 nucleotides of 3′ untranslated sequence. Two overlapping polyadenylation signals (AATAAA) are present 10 to 20 nucleotides upstream from the 31 adenylic acid residues at the 3′ end of the clone. A 9-nucleotide repeat (ACCCCAGGC) is present at positions 202 to 210 and 211 to 219.
Features of the Deduced Protein:
The pAP1 open reading frame encodes a 119-amino acid deduced polypeptide with a predicted mass of 13 kD and a calculated isoelectric point of 10.2. The subcellular location has not been determined.
Chromosomal Localization:
Unknown, according to Southern data, gene copy number is low.

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The GenBank/EMBL accession number for the sequence reported in this article is L15194.

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